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ABSTRACT OF THE DISCLOSURE

A method for gene mapping from genotype and phenotype data utilizes linkage disequilibrium between genetic markers m_i , which are polymorphic nucleic acid or protein sequences or strings of single-nucleotide polymorphisms deriving from a chromosomal region. All marker patterns P that satisfy a certain pattern evaluation function $e(P)$ are searched from the data, each marker m_i of the data is scored by a marker score and the location of the gene is predicted as a function of the scores $s(m_i)$ of all the markers m_i in the data.